



BLASTP 2.2.1 [Apr-13-2001]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

BID: 1003946835-11427-26633

Query=

(10 letters)

CATDIKGATC circular

Database: nr

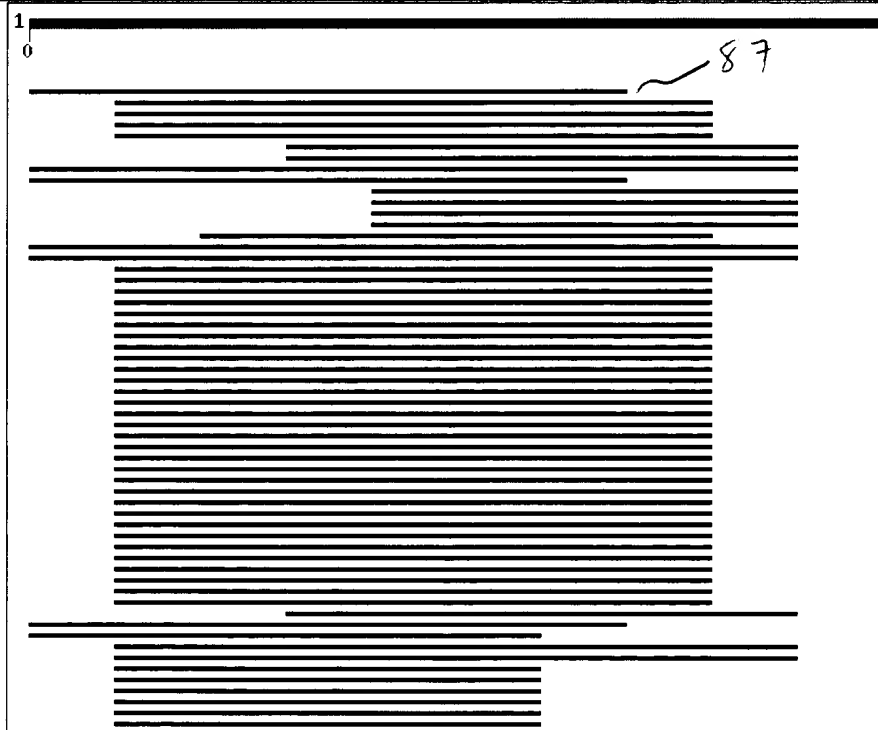
777,663 sequences; 247,121,334 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Score E

10 24:01 2:10 PM

gi 1781643 gb AA097445.1	(U58841) pilin [Neisseria gonorrhoea...]	21	1058
gi 441614 gb AA01245.1	(AF042049) beta-1,4-xylosidase [L...	21	1058
gi 446414 gb AA01412.1	(L28140) pilin [Neisseria gonorrhoea...]	21	1058
gi 466114 gb AA01664.1	(L28140) pilin [Neisseria gonorrhoea...]	21	1058
gi 1151177 gb AA01764.1	ShkA1 pilin [Neisseria gonorrhoea...]	21	1058
gi 116431 pir S13307	nerve growth factor - monocled cobra ...	21	1058
gi 2810153 gb AA02011.1 AF174111.1	(AF173253) selenophosph...	21	1058
gi 1604177 gb AA01412.1	L28140 pilin [Neisseria gonorrhoea...]	21	1058
gi 1151177 sp P21177	NGF NERVE GROWTH FACTOR (NGF)	21	1058
gi 1151177 gb AA01744.1	(U58841) pilin [Neisseria gonorrhoea...]	21	1058
gi 447661 sp P44118	NGF BDNF NERVE GROWTH FACTOR RECEPTOR...	21	1058
gi 1151177 pir S13307	nerve growth factor beta chain prec...	21	1058
gi 1151177 gb AA01412.1	(AF14084) envelope glycoprotein...	21	1058
gi 447661 emb AC00416.1	AG1160f membrane tyrosine pro...	21	1058
gi 1501333 gb AA01664.1	M16013 gonococcal pilin protein ...	21	1058
gi 14712416 ref NP_001556.2	hypothetical protein XP_001556...	21	1058
gi 1501333 gb AA01664.1 AF164111.1	(AF164129) OFF154 [w...	21	1058
gi 1501333 emb CA04456.2	(AC178063) selenophosphate synt...	21	1058
gi 1501333 gb AA01664.1	(AF14084) beta-1,4-xylosidase [L...	21	1058
gi 1501333 ref NP_001556.1	Glycerol-3-P dehydrogenase [Ch...	21	1058
gi 1501333 ref NP_001556.1	beta-1,4-xylosidase (EC 3.2.1....)	21	1058
gi 1501333 gb AA01664.1	(AF14084) pilus subunit [Neisser...	21	1058
gi 1501333 ref NP_001556.1	hypothetical protein FLJ13078 (...)	21	1058
gi 1501333 gb AA01664.1	(AF14084) pilus subunit [Neisser...	21	1058
gi 1501333 gb AA01664.1	(U58841) pilin [Neisseria gonorrhoea...]	21	1058
gi 1501333 gb AA01664.1	(AF14084) pilus subunit [Neisser...	21	1058
gi 1501333 ref NP_001556.1	quinone oxidoreductase [Bacill...	21	1058
gi 1501333 pir S13307	nerve growth factor - Naja naja xgi7...	21	1058
gi 1501333 gb AA01664.1	(U58841) pilin [Neisseria gonorrhoea...]	21	1058
gi 1501333 sp P01140	NGF NERVE GROWTH FACTOR (NGF)	21	1058
gi 1501333 ref NP_001556.1	putative beta-galactosidase [A...	21	1470
gi 1501333 sp P01140	L-ASPARAGINASE (L-ASPARAGINE...	21	1470
gi 1501333 gb AA01664.1 AF169053.1	(AF169053) 20S proteaso...	21	1470
gi 1501333 pir S13307	potassium channel protein Slo - fruit...	21	1470
gi 1501333 ref NP_001556.1	unknown protein [Arabidopsis t...	21	1470
gi 1501333 pir S13307	calcium-activated potassium channel, ...	21	1470
gi 1501333 emb AC00416.1	AJ11686 transcription factor ...	21	1470

Alignments

```

>gi|4142176|gb|AF073824.1| (U30306) T-cell receptor alpha V-J junction [Homo sapiens]
      Length: 14

```

Score = 23.5 bits (4%), Expect = 161
Identities = 7/8 (87%), Positives = 7/8 (87%)

```
Query: 1 CATDIRGA 5
      CATDIRGA
Skip: 2 CATDIRGA 4
```

gi|14339434|env02AC04_618.11 (AF14790) putative zinc finger protein [Homo sapiens]
length = 167

Score = 21.7 bits (44%), Expect = 326
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 4 DINGBEE 10
DING EE
Sbjct: 49' DINGBEE 500

gi_4423631.gb|AA10416.1 AF10358) outer surface protein C precursor [Morreita sp.
Length = 31.

Score = 31.7 bits (46%), Expect = 327
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDIKGAE 9
 ATDIKGAE
 Subject: 164 ATDIKGAE 171

Date

gi|128165|sp|P_0675|NGF_PRANA BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)
 Length = 241

Score = 22.7 bits (46), Expect = 3.26
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 ATDIKGAE 4
 ATDIKGAE
 Subject: 144 ATDIKGAE 186

gi|69054|pir|NGFRA nerve growth factor beta chain precursor - multimammate rat
 (Mastomys natalensis)
gi|202115|gb|AA040899.1| (M22743) nerve growth factor [Mastomys natalensis]
 Length = 373

Score = 22.7 bits (46), Expect = 3.26
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 ATDIKGAE 4
 ATDIKGAE
 Subject: 111 ATDIKGAE 118

gi|14712329|ref|XP_044985.1| hypothetical protein XP_044985 [Homo sapiens]
 Length = 603

Score = 22.7 bits (46), Expect = 3.26
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 4 DIKGAE 19
 DIKGAE
 Subject: 119 DIKGAE 5.1

gi|15608363|ref|NP_47159.1| SSU ribosomal protein S11P (rpsK) [Methanococcus janna
gi|1710719|sp|P54031|RS11 METUA 30S RIBOSOMAL PROTEIN S11P
gi|119051|pir|H69503|ribosomal protein S11 - Methanococcus jannaschii
gi|1593936|gb|AA035171.1| (U67475) SSU ribosomal protein S11P (rpsK) [Methanococcus
jannaschii]
 Length = 119

Score = 22.7 bits (46), Expect = 3.26
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 ATDIKGAE 9
 ATDIKGAE
 Subject: 25 ATDIKGAE 32

gi|16113334|ref|NP_406647.1| 4-methyl-5(B-hydroxyethyl)-thiazol monophosphate biosy
enzyme [Yersinia pestis]
gi|1594111|ref|CAC3407.1| (AJ41415) 4-methyl-5(B-hydroxyethyl)-thiazol monophosp
biosynthesis enzyme [Yersinia pestis]
 Length = 146

Score = 22.3 bits (45), Expect = 4.38
 Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 1 IKGAET 10
 IKGAET
 Subject: 76 IKGAET 81

Date

gi|15800174|ref|NP_286166.1| 4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate s

[Escherichia coli O157:H7 EDL933]
 gi|15829732|ref|NP_308515.1| 4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate s
 [Escherichia coli O157:H7]
 gi|12513210|gb|AA054774.1|AF005221.1| AE005221| 4-methyl-5(beta-hydroxyethyl)-thia
 zole synthesis [Escherichia coli O157:H7 EDL933]
 gi|13359455|bj|BA033001.1| (AP002551) 4-methyl-5(beta-hydroxyethyl)-thiazole monoph
 osphate synthesis [Escherichia coli O157:H7]
 Length = 195

Score = 21.3 bits (45), Expect = 43e-
 Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 1 IKGAEC 11
 IKGAEC
 Subject: 78 IKGAEC 33

>gi|7517613|pir|T37201 Notch homolog protein - sea squirt (Halocynthia roretzi)
 gi|3940867|gb|BA015571.1| (AB011327) HsNotch protein [Halocynthia roretzi]
 Length = 2352

Score = 21.3 bits (45), Expect = 43e-
 Identities = 7/10 (70%), Positives = 7/10 (70%), Gaps = 2/10 (20%)

Query: 1 CATIKGAEC 10
 CATI EC
 Subject: 991 CATIIN--EC 798

>gi|6680341|sp|Q46248|THI1 ECOLI 4-METHYL-5(B-HYDROXYETHYL)-THIAZOLE MONOPHOSPHATE B
 ENZYME
 Length = 196

Score = 21.3 bits (45), Expect = 43e-
 Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 5 IKGAEC 10
 IKGAEC
 Subject: 76 IKGAEC 31

>gi|16128409|ref|NP_414263.1| 4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate s
 [Escherichia coli K12]
 gi|7424595|pir|H64771 hydroxymethylpyrimidine kinase (EC 2.7.1.49) - Escherichia c
 gi|1100871|gb|AA057734.1| (U04903) ThiC [Escherichia coli]
 gi|1773183|gb|AB040130.1| (U08064) 4-methyl-5(beta-hydroxyethyl)-thiazole monophosphat
 e biosynthesis protein [Escherichia coli]
 gi|1780616|gb|AAC73527.1| (AE000143) 4-methyl-5(beta-hydroxyethyl)-thiazole monopho
 sphate synthesis [Escherichia coli K12]
 Length = 195

Score = 21.3 bits (45), Expect = 43e-
 Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 5 IKGAEC 10
 IKGAEC
 Subject: 78 IKGAEC 33

>gi|1242611|cds|LF00_B Chain B, Molecular: Structure Of A High Potential Cytochrome C
 Isolated From Rhodospila Globiformis
 gi|1242611|cds|LF00_A Chain A, Molecular: Structure Of A High Potential Cytochrome C
 Isolated From Rhodospila Globiformis
 Length = 105

Score = 21.3 bits (45), Expect = 43e-
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 CATIKGA 8

C TDIKGA

Sbjct: 22 CHTDIKGA 29

gi|14583855|gb|AAK01629.1| (AY037148) phosphatidylethanolamine binding protein [Homo
Length = 117

Score = 21.8 bits (44), Expect = 588
 Identities = 6/7 (86%), Positives = 7/7 (89%)

Query: 3 TDIKGAE 3
 TDIKGA+
 Sbjct: 119 TDIKGAD 122

gi|15012803|gb|AAH11123.1|AAH11123 (58011123) Similar to nerve growth factor, beta
Length = 124

Score = 21.4 bits (42), Expect = 712
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDIKGA E
 ATDIK E
 Sbjct: 215 ATDIKGE 212

gi|2305312|ref|NP_035637.1| nerve growth factor, beta [Mus musculus]
gi|69053|gir|NGMSMG nerve growth factor beta chain precursor - mouse
gi|51305|emb|CAAG4111.1| (V00936) precursor of NGF [Mus musculus]
gi|300684|gb|AAA39411.1| (M14808) nerve growth factor beta [Mus musculus]
gi|337171|gb|AAA37646.1| (M17398) nerve growth factor [Mus musculus]
gi|337444|gb|AAA39411.1| (M35773) nerve growth factor [Mus musculus]
gi|337444|gb|AAA39411.1| (E01719) prepro-beta-nerve growth factor [Mus musculus]
gi|467311|gb|AAA37647.1| (M17106) nerve growth factor [Mus musculus]
gi|235450|prf|1385134A nerve growth factor precursor [Mus musculus]
Length = 127

Score = 21.4 bits (42), Expect = 784
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDIKGA E
 ATDIK E
 Sbjct: 215 ATDIKGE 212

gi|69051|gir|NGHUBM nerve growth factor beta chain precursor - human (fragment)
gi|23053|prf|1385137A nerve growth factor beta [Homo sapiens]
Length = 126

Score = 21.4 bits (42), Expect = 784
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDIKGA E
 ATDIK E
 Sbjct: 194 ATDIKGE 201

gi|112441|gb|AA46844.1| (M26810) nerve growth factor [Gallus gallus]
Length = 113

Score = 21.4 bits (42), Expect = 784
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDIKGA E
 ATDIK E
 Sbjct: 21 ATDIKGE 34

gi|84671|gir|A2631 nerve growth factor beta chain precursor - bovine (fragment)
gi|163410|gb|AAA30688.1| (M26809) nerve growth factor [Bos taurus]
Length = 123

Score = 21.4 bits (43), Expect = 7e-9
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDIKGAEE
 ATDIKGE
 Subject: 33 ATDIKSGKE 40

gi|4245742|gb|AA0266.3.2| S62039) nerve growth factor [Mus sp.]
 Length = 171

Score = 21.4 bits (43), Expect = 7e-9
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 3 ATDIKGAEE
 ATDIKGE
 Subject: 149 ATDIKSGKE 136

gi|111553|pir|I156570 beta-nerve growth factor - rat (fragment)
gi|105622|gb|AA04109.1| (M36589) beta-nerve growth factor [Rattus norvegicus]
 Length = 148

Score = 21.4 bits (43), Expect = 7e-9
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 4 ATDIKGAEE
 ATDIKGE
 Subject: 153 ATDIKSGKE 160

gi|4306391|ref|NP_01497.1 nerve growth factor, beta polypeptide; Nerve growth fac
 [Homo sapiens]
gi|128161|sp|P01138 NGF HUMAN BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)
gi|124377|emb|C3A36832.1| (X52399) beta nerve growth factor (AA 1-241) [Homo sapiens]
gi|119303|gb|AA09901.1| (M21962) nerve growth factor beta [Homo sapiens]
gi|107198|emb|CA024315.1| (V01511) beta-nerve growth factor [Homo sapiens]
 Length = 141

Score = 21.4 bits (43), Expect = 7e-9
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 5 ATDIKGAEE
 ATDIKGE
 Subject: 149 ATDIKSGKE 136

gi|30417.4|sp|P13600 NGF BOVIN BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)
gi|138-7|0|emb|CA07059.1| (Y09566) beta-nerve growth factor [Bos taurus]
 Length = 231

Score = 21.4 bits (43), Expect = 7e-9
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 6 ATDIKGAEE
 ATDIKGE
 Subject: 139 ATDIKSGKE 146

gi|121616|pdb|1SGFY Chain Y, Crystal Structure Of 7s Ngf: A Complex Of Nerve Grow
 Factor With Four Binding Proteins (Serine Proteinases)
gi|121616|5|pdb|1SGFB Chain B, Crystal Structure Of 7s Ngf: A Complex Of Nerve Grow
 Factor With Four Binding Proteins (Serine Proteinases)
 Length = 116

Score = 21.4 bits (43), Expect = 7e-9
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 7 ATDIKGAEE

ATDING E
 Subject: 28 ATDINGKE 35

gi|4034770|sp|P21617|NGF_XENLA NERVE GROWTH FACTOR PRECURSOR (NGF)
 Length = 131

Score = 21.4 bits (43), Expect = 789
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 ATDINGKE 9
 ATDING E
 Subject: 141 ATDINGKE 143

gi|1351445|sp|F2547|NGF_RAT BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)
 Length = 131

Score = 21.4 bits (43), Expect = 789
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 ATDINGKE 9
 ATDING E
 Subject: 149 ATDINGKE 155

gi|128150|sp|F05000|NGF_CHICK BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)
 Length = 145

Score = 21.4 bits (43), Expect = 789
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 ATDINGKE 9
 ATDING E
 Subject: 151 ATDINGKE 159

gi|1361674|ref|XP_002122.2| nerve growth factor, beta polypeptide [Homo sapiens]
gi|16116835|ref|XP_054005.1| hypothetical protein XP_058005 [Homo sapiens]
gi|5917605|gb|AA053405.1|AF150960.1 (AF150960) nerve growth factor B [Homo sapiens]
gi|7018400|emb|CAB2425.1| (AL049325) dJ662B22.1 (nerve growth factor, beta polypep
 sapiens)
 Length = 141

Score = 21.4 bits (43), Expect = 789
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 ATDINGKE 9
 ATDING E
 Subject: 149 ATDINGKE 155

gi|6815207|dbj|BAAN0438.1 (AB037518) beta-nerve growth factor [Pan troglodytes]
 Length = 141

Score = 21.4 bits (43), Expect = 789
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 1 ATDINGKE 9
 ATDING E
 Subject: 149 ATDINGKE 155

gi|1561175|ref|NP_223326.1| CHORISMATE SYNTHASE [Helicobacter pylori J99]
gi|11151448|sp|Q6ZLH1|AROC_HELPJ CHORISMATE SYNTHASE (5-ENOLPYRUVYLSHIKIMATE-3-PHOS
 PHOSPHOLYASE)
gi|743723|pir|F71911 chorismate synthase - Helicobacter pylori (strain J99)
gi|4158160|gb|AA08159.1 (AE001492) CHORISMATE SYNTHASE [Helicobacter pylori J99]
 Length = 565

Score = 21.4 bits (43), Expect = 789

Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 4 DIKGAEC 1
DIKG EC
Sbjct: 303 DIKGNEC 315

gi|6815209|dbj|BAI4439.1| (AB037519) beta-nerve growth factor [Gorilla gorilla]
Length = 151

Score = 11.4 bits (43), Expect = 789
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 5 ATDIKGAEC 9
ATDIKG E
Sbjct: 149 ATDIKGE 156

gi|14164981|gb|AAK55325.1|AF355457.1 (AF355457) thaumatin-like protein TLP7 [Hordeu
Length = 157

Score = 11.4 bits (43), Expect = 789
Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query: 6 CATDI-KGAEC 10
CATDI K EC
Sbjct: 145 CATDITK--EC 153

gi|2490137|sp|Q29004 NGF PIG BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)
gi|7136538|pir|I45613 nerve growth factor B - pig (fragment)
gi|833771|gb|AAAL100.1| (L31898) nerve growth factor B [Sus scrofa]
Length = 157

Score = 11.4 bits (43), Expect = 789
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 7 ATDIKGAEC 9
ATDIKG E
Sbjct: 137 ATDIKGE 144

gi|86383|pir||A26311 nerve growth factor beta chain precursor - chicken (fragment)
gi|1334740|emb|CAAF7633.1 (X04003) prepro-polypeptide (aa -123 to 118); gtg start
gallus]
Length = 148

Score = 11.4 bits (43), Expect = 789
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 8 ATDIKGAEC 9
ATDIKG E
Sbjct: 157 ATDIKGE 169

gi|8157159|gb|AAB341.4.2| (S76884) truncated beta nerve growth factor; beta-NGF [Ho
sapiens]
Length = 157

Score = 11.4 bits (43), Expect = 789
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 9 ATDIKGAEC 9
ATDIKG E
Sbjct: 28 ATDIKGE 36

gi|126161|sp|F01130|NGF MOUSE BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)
Length = 151

Score = 11.4 bits (43), Expect = 789

Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDINGAE 9
ATDING E
Sbjct: 143 ATDINGKE 156

gi|127545|pcb|1WWW.W Chain W, Ngf In Complex With Domain 5 Of The Trka Receptor
gi|127544|pcb|1WWW.V Chain V, Ngf In Complex With Domain 5 Of The Trka Receptor
gi|108434|gb|AA73805.1| (M30504) nerve growth factor [synthetic construct]
Length = 126

Score = 11.4 bits (43), Expect = 784
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDINGAE 9
ATDING E
Sbjct: 28 ATDINGKE 35

gi|1818711|cds|BAAC0440.1| (AB037520) beta-nerve growth factor [Pongo pygmaeus]
Length = 141

Score = 11.4 bits (43), Expect = 784
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDINGAE 9
ATDING E
Sbjct: 143 ATDINGKE 156

gi|122411|cds|AA00008.1| (D00010) beta-nerve growth factor [Gallus gallus]
gi|105734|cds|AA00008.1| (X04067) pro-beta-nerve growth factor (aa 1-126) [Gallus
Length = 126

Score = 11.4 bits (43), Expect = 784
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDINGAE 9
ATDING E
Sbjct: 35 ATDINGKE 41

gi|104144|pir|S14481 nerve growth factor beta chain precursor - African clawed frog
gi|14919|emb|CAA39140.1| (X55716) nerve growth factor prepropeptide [Xenopus laevis]
Length = 130

Score = 11.4 bits (43), Expect = 784
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDINGAE 9
ATDING E
Sbjct: 143 ATDINGKE 156

gi|1442172|pir|T04470 perml protein - barley (fragment)
gi|1454602|gb|AA071670.1| (AF016327) Barperml [Hordeum vulgare]
Length = 100

Score = 11.4 bits (43), Expect = 784
Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query: 1 CATDIFGAE 10
CATDIF EC
Sbjct: 123 CATDITF--EC 131

gi|126154|sp|P1909A|NGF CAUPO BETA-NERVE GROWTH FACTOR PRECURSOR (BETA-NGF)
gi|103006|pir|JL0007 nerve growth factor beta chain precursor - guinea pig
Length = 241

Score = 11.4 bits (43), Expect = 789
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDINGAE 9
 ATDING E
 Sbjct: 14 ATDINGKE 156

gi|631524|gb|BA90437.1| (AB037517) beta-nerve growth factor [Homo sapiens]
 Length = 241

Score = 11.4 bits (43), Expect = 789
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDINGAE 9
 ATDING E
 Sbjct: 14 ATDINGKE 156

gi|6969512|gb|AA033730.1|AF222632.1 (AF222632) beta nerve growth factor [Macaca fus]
 Length = 117

Score = 11.4 bits (43), Expect = 789
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDINGAE 9
 ATDING E
 Sbjct: 139 ATDINGKE 146

gi|1431713|pdb|1PTG A Chain A, Crystal Structure Of Beta Nerve Growth Factor At 2.5
 Resolution In C2 Space Group With Zn Ions Bound
gi|1431716|pdb|1PTG B Chain B, Crystal Structure Of Beta Nerve Growth Factor At 2.5
 Resolution In C2 Space Group With Zn Ions Bound
gi|1431717|pdb|1PTG C Chain C, Crystal Structure Of Beta Nerve Growth Factor At 2.5
 Resolution In C2 Space Group With Zn Ions Bound
 Length = 110

Score = 11.4 bits (43), Expect = 789
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDINGAE 9
 ATDING E
 Sbjct: 10 ATDINGKE 17

gi|656412|gb|AA014335.1|AF145043.1 (AF145043) beta nerve growth factor [Cervus ela]
 Length = 87

Score = 11.4 bits (43), Expect = 789
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDINGAE 9
 ATDING E
 Sbjct: 13 ATDINGKE 19

gi|576004|pdb|1BET Beta-Nerve Growth Factor
 Length = 107

Score = 11.4 bits (43), Expect = 789
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 2 ATDINGAE 9
 ATDING E
 Sbjct: 19 ATDINGKE 16

gi|15703413|gb|AA015874.1|AF411526.1 (AF411526) nerve growth factor beta [Homo sapi]
 Length = 241

Score = 41.4 bits (43), Expect = 789
 Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 3 ATDINGAE 9
 ATDING E
 Subject: 140 ATDINGKE 156

gi|1291606|gb|AA052918.1| (AE063628) ops2 gene product [Drosophila melanogaster]
 Length = 515

Score = 41.0 bits (42), Expect = 105
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 1 CATDING 7
 CATDING G
 Subject: 100 CATDITG 216

gi|15793124|ref|NP_253104.1| truncated pilin [Neisseria meningitidis Z2491]
gi|11287672|ref|EF0121 truncated pilin NMA0266 [imported] - Neisseria meningitidis
 (group A strain Z2491)
gi|1374014|emb|CAB63374.1| (AL162752) truncated pilin [Neisseria meningitidis Z2491]
 Length = 141

Score = 21.0 bits (41), Expect = 105
 Identities = 5/6 (100%), Positives = 5/6 (100%)

Query: 3 ATDING 7
 ATDING
 Subject: 14 ATDING 59

Database: nr
 Posted date: Oct 23, 2001 6:02 PM
 Number of letters in database: 247,121,334
 Number of sequences in database: 777,863

Lambda	K	H
0.355	0.149	1.83

Gapped		
Lambda	K	H
0.294	0.110	0.610

Matrix: BAM30
 Gap Penalties: Existence: 9, Extension: 1
 Number of Hits to DB: 7,358,637
 Number of Sequences: 777663
 Number of extensions: 59715
 Number of successful extensions: 1516
 Number of sequences better than 20000.0: 1509
 Number of HSP's better than 20000.0 without gapping: 1509
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
 Number of HSP's gapped (non-prelim): 1516
 length of query: 10
 length of database: 247,121,334
 effective HSP length: 1
 effective length of query: 9
 effective length of database: 246,343,071
 effective search space: 2217093039
 effective search space used: 2217093039
 T: 11
 A: 40
 X1: 14 (7.1 bits)
 X2: 35 (14.5 bits)

X3: 58 (24.6 bits)
S1: 33 (18.7 bits)
S2: 33 (17.2 bits)